RAW SEQUENCE LISTING
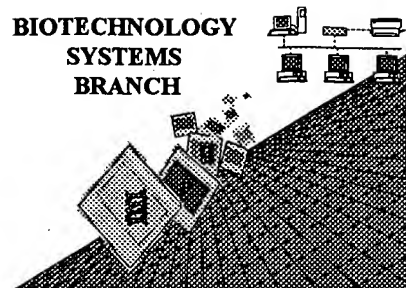# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: *09/210,952*

Art Unit / Team No. : *OIPE*

Date Processed by STIC: *12/23/98*

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/210,952_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.

4 _____ Misaligned Amino Acid . The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
       Numbering   between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

1 2, 3 4 /5 (maybe more)

6 _____ Variable Length
Sequence(s) _1_ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.

7 _____ Wrong Designation
Sequence(s) _____ contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)

8 _____ Skipped Sequences
       (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xI) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences
       (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of N's or Xaa's
        (NEW RULES)
Use of N's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

11 _____ Use of <213>Organism
        (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature
        (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)

13 _____ Wrong Format
File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the
"Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures"
Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620
applies to applications filed on or after July 1, 1998.

AKS-Biotechnology Systems Branch- 7/10/98

> This Raw Listing contains the General Information
> Section and up to first 5 pages.

*sup. 5
new format*

Corrected Diskette Needed   Does Not Comply

```
 1   <110> APPLICANT: Fainzilber, Michael M.
 2         Kits, Karel S.
 3         Burlingame, Alma L.
 4         Olivera, Baldomero M.
 5         Walker, Craig
 6         Watkins, Maren
 7         Shetty, Reshma
 8         Cruz, Lourdes J.
 9         Imperial, Julita
10         Colledge, Clark
11         University of Utah Resarch Foundation
12         Vrije Universiteit
13         Regents of the University of California
14   <120> TITLE OF INVENTION: Gamma-Conopeptides
15   <130> FILE REFERENCE: Gamma-Conpeptides
16   <140> CURRENT APPLICATION NUMBER: US/09/210,952
17   <141> CURRENT FILING DATE: 1998-12-15
18   <150> EARLIER APPLICATION NUMBER: US 60/069,706
19   <151> EARLIER FILING DATE: 1997-12-16
20   <160> NUMBER OF SEQ ID NOS: 47
21   <170> SOFTWARE: PatentIn Ver. 2.0
22   <210> SEQ ID NO 1
23   <211> LENGTH: 13
24   <212> TYPE: PRT
25   <213> ORGANISM: Artificial Sequence
26   <220> FEATURE:
27   <223> OTHER INFORMATION: Description of Artificial Sequence:generic formula
28         of gamma-conopeptides
29   <220> FEATURE:
30   <221> NAME/KEY: PEPTIDE
31   <222> LOCATION: (1)
32   <223> OTHER INFORMATION: Xaa at residue 1 is des-Xaa or a peptide having
33         1-6 amino acids.
34   <220> FEATURE:
35   <221> NAME/KEY: PEPTIDE
36   <222> LOCATION: (3)
37   <223> OTHER INFORMATION: Xaa at residue 3 is a peptide having 5-6 amino
38         acids.
39   <220> FEATURE:
40   <221> NAME/KEY: PEPTIDE
41   <222> LOCATION: (5)
42   <223> OTHER INFORMATION: Xaa at residue 5 is a peptide having 4 amino
43         acids.
44   <220> FEATURE:
```

invalid — see item 6 on Error summary sheet

same error

same

```
45   <221> NAME/KEY: PEPTIDE                         OK
46   <222> LOCATION: (6)
47   <223> OTHER INFORMATION: Xaa at residue 6 is Glu, gamma-carboxylglutamate
48         or Gln.
49   <220> FEATURE:
50   <221> NAME/KEY: PEPTIDE                      error
51   <222> LOCATION: (9)
52   <223> OTHER INFORMATION: Xaa at residue 9 is a peptide having 3-4 amino
53         acids.
54   <220> FEATURE:
55   <221> NAME/KEY: PEPTIDE                      error
56   <222> LOCATION: (11)
57   <223> OTHER INFORMATION: Xaa at residue 11 is a peptide having 3-6 amino
58         acids.
59   <220> FEATURE:
60   <221> NAME/KEY: PEPTIDE                   error
61   <222> LOCATION: (13)
62   <223> OTHER INFORMATION: Xaa at residue 13 is des-Xaa or a peptide of 2-9
63         amino acids.
64   <400> SEQUENCE: 1                    OK
65   Xaa Cys Xaa Cys Xaa Xaa Cys Cys Xaa Cys Xaa Cys Xaa
66    1               5                  10
67   <210> SEQ ID NO 2
68   <211> LENGTH: 14
69   <212> TYPE: PRT
70   <213> ORGANISM: Artificial Sequence
71   <220> FEATURE:
72   <223> OTHER INFORMATION: Description of Artificial Sequence:generic
73         sequence of gamma-conopeptides.
74   <220> FEATURE:
75   <221> NAME/KEY: PEPTIDE           same error on seq 1
76   <222> LOCATION: (1)
77   <223> OTHER INFORMATION: Xaa at residue 1 is des-Xaa or a peptide having
78         1-6 amino acids.
79   <220> FEATURE:
80   <221> NAME/KEY: PEPTIDE                      same
81   <222> LOCATION: (3)
82   <223> OTHER INFORMATION: Xaa at residue 3 is a peptide having 5-6 amino
83         acids.
84   <220> FEATURE:
85   <221> NAME/KEY: PEPTIDE                      same
86   <222> LOCATION: (5)
87   <223> OTHER INFORMATION: Xaa at residue 5 is a peptide having 4 amino
88         acids.
89   <220> FEATURE:
90   <221> NAME/KEY: PEPTIDE                    OK
91   <222> LOCATION: (6)
92   <223> OTHER INFORMATION: Xaa at residue 6 is Glu, gamma-carboxyglutamate or
93         Gln.
94   <220> FEATURE:
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W--> (line 65)

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 95    <221> NAME/KEY: PEPTIDE                    OK
 96    <222> LOCATION: (9)
 97    <223> OTHER INFORMATION: Xaa at residue 9 is Ser or Thr.
 98    <220> FEATURE:
 99    <221> NAME/KEY: PEPTIDE                        erra
100    <222> LOCATION: (10)
101    <223> OTHER INFORMATION: Xaa at residue 10 is a peptide having 2-3 amino
102          acids.
103    <220> FEATURE:
104    <221> NAME/KEY: PEPTIDE
105    <222> LOCATION: (12)                               erra
106    <223> OTHER INFORMATION: Xaa at residue 12 is a peptide having 3-6 amino
107          acids.
108    <220> FEATURE:
109    <221> NAME/KEY: PEPTIDE
110    <222> LOCATION: (14)                               erra
111    <223> OTHER INFORMATION: Xaa at residue 14 is a peptide having 2-9 amino
112          acids.
113    <400> SEQUENCE: 2                    OK
W-->114    Xaa Cys Xaa Cys Xaa Xaa Cys Cys Xaa Xaa Cys Xaa Cys Xaa
115     1                   5                  10
116    <210> SEQ ID NO 3
117    <211> LENGTH: 16
118    <212> TYPE: PRT
119    <213> ORGANISM: Artificial Sequence
120    <220> FEATURE:
121    <223> OTHER INFORMATION: Description of Artificial Sequence:generic formula
122          of gamma-conopeptides
123    <220> FEATURE:
124    <221> NAME/KEY: PEPTIDE
125    <222> LOCATION: (1)                            erra
126    <223> OTHER INFORMATION: Xaa at residue 1 is a peptide having 1-6 amino
127          acids.
128    <220> FEATURE:
129    <221> NAME/KEY: PEPTIDE       "Xaa" can only represent a single amino
130    <222> LOCATION: (3)                                      acid, nothing
131    <223> OTHER INFORMATION: Xaa at residue 3 is a hexapeptide.            else.
132    <220> FEATURE:
133    <221> NAME/KEY: PEPTIDE
134    <222> LOCATION: (5)                            erra
135    <223> OTHER INFORMATION: Xaa at residue 5 is a peptide having 4 amino
136          acids.
137    <220> FEATURE:
138    <221> NAME/KEY: PEPTIDE
139    <222> LOCATION: (6)                            OK
140    <223> OTHER INFORMATION: Xaa at residue 6 is Glu or gamma-carboxyglutamate.
141    <220> FEATURE:
142    <221> NAME/KEY: PEPTIDE
143    <222> LOCATION: (14)
144    <223> OTHER INFORMATION: Xaa at residue 14 is a tripeptide.
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```
145    <220> FEATURE:
146    <221> NAME/KEY: PEPTIDE
147    <222> LOCATION: (16)
148    <223> OTHER INFORMATION: Xaa at residue 16 is a peptide having 7-9 amino
149          acids.
150    <400> SEQUENCE: 3
151    Xaa Cys Xaa Cys Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Cys Xaa
152     1               5                   10                  15
153    <210> SEQ ID NO 4
154    <211> LENGTH: 17
155    <212> TYPE: PRT
156    <213> ORGANISM: Artificial Sequence
157    <220> FEATURE:
158    <223> OTHER INFORMATION: Description of Artificial Sequence:generic
159          sequence of gamma-conopeptides.
160    <220> FEATURE:
161    <221> NAME/KEY: PEPTIDE
162    <222> LOCATION: (1)
163    <223> OTHER INFORMATION: Xaa at residue 1 is a peptide having 1-6 amino
164          acids.
165    <220> FEATURE:
166    <221> NAME/KEY: PEPTIDE
167    <222> LOCATION: (3)
168    <223> OTHER INFORMATION: Xaa at residue 3 is a hexapeptide.
169    <220> FEATURE:
170    <221> NAME/KEY: PEPTIDE
171    <222> LOCATION: (5)
172    <223> OTHER INFORMATION: Xaa at residue 5 is Ser or Thr.
173    <220> FEATURE:
174    <221> NAME/KEY: PEPTIDE
175    <222> LOCATION: (6)
176    <223> OTHER INFORMATION: Xaa at residue 6 is a tripeptide.
177    <220> FEATURE:
178    <221> NAME/KEY: PEPTIDE
179    <222> LOCATION: (7)
180    <223> OTHER INFORMATION: Xaa at residue 7 is Glu or gamma-carboxyglutamate.
181    <220> FEATURE:
182    <221> NAME/KEY: PEPTIDE
183    <222> LOCATION: (15)
184    <223> OTHER INFORMATION: Xaa at residue 15 is a tripeptide.
185    <220> FEATURE:
186    <221> NAME/KEY: PEPTIDE
187    <222> LOCATION: (17)
188    <223> OTHER INFORMATION: Xaa at residue is a peptide having 7-9 amino
189          acids.
190    <400> SEQUENCE: 4
191    Xaa Cys Xaa Cys Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Cys
192                     5                   10                  15
193    Xaa
194    <210> SEQ ID NO 5
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195    <211> LENGTH: 26
196    <212> TYPE: PRT
197    <213> ORGANISM: Artificial Sequence
198    <220> FEATURE:
199    <223> OTHER INFORMATION: Description of Artificial Sequence:generic
200          sequence of gamma-conopeptides.
201    <220> FEATURE:
202    <221> NAME/KEY: PEPTIDE
203    <222> LOCATION: (1)
204    <223> OTHER INFORMATION: Xaa at residue 1 is des-Xaa or a dipeptide.
205    <220> FEATURE:
206    <221> NAME/KEY: PEPTIDE
207    <222> LOCATION: (2)
208    <223> OTHER INFORMATION: Xaa at residue 2 is Asp, Glu or
209          gamma-carboxyglutamate.
210    <220> FEATURE:
211    <221> NAME/KEY: PEPTIDE
212    <222> LOCATION: (4)
213    <223> OTHER INFORMATION: Xaa at residue 4 is a dipeptide.
214    <220> FEATURE:
215    <221> NAME/KEY: PEPTIDE
216    <222> LOCATION: (5)
217    <223> OTHER INFORMATION: Xaa at residue 5 is Trp or 6-bromo-Trp.
218    <220> FEATURE:
219    <221> NAME/KEY: PEPTIDE
220    <222> LOCATION: (7)
221    <223> OTHER INFORMATION: Xaa at residue 7 is dipeptide.
222    <220> FEATURE:
223    <221> NAME/KEY: PEPTIDE
224    <222> LOCATION: (10)
225    <223> OTHER INFORMATION: Xaa at residue 10 is a dipeptide.
226    <220> FEATURE:
227    <221> NAME/KEY: PEPTIDE
228    <222> LOCATION: (12)
229    <223> OTHER INFORMATION: Xaa at residue 12 is Glu, gamma-carboxyglutamate
230          or Gln.
231    <220> FEATURE:
232    <221> NAME/KEY: PEPTIDE
233    <222> LOCATION: (24)
234    <223> OTHER INFORMATION: Xaa at residue 24 is any amino acid.
235    <220> FEATURE:
236    <221> NAME/KEY: PEPTIDE
237    <222> LOCATION: (26)
238    <223> OTHER INFORMATION: Xaa at residue 26 is a pentapeptide.
239    <400> SEQUENCE: 5
240       Xaa Xaa Cys Xaa Xaa Phe Xaa Cys Thr Xaa Ser Xaa Cys Cys Ser Asn
241        1              5              10             15
242       Ser Cys Asp Trp Thr Tyr Cys Xaa Leu Xaa
243               20             25
244    <210> SEQ ID NO 6
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Line	?	Error/Warning	Original Text
65	W	"N" or "Xaa" used: Feature required	Xaa Cys Xaa Cys Xaa Xaa Cys Cys Xaa Cys X
114	W	"N" or "Xaa" used: Feature required	Xaa Cys Xaa Cys Xaa Xaa Cys Cys Xaa Xaa C
151	W	"N" or "Xaa" used: Feature required	Xaa Cys Xaa Cys Xaa Xaa Cys Cys Ser Asn S
191	W	"N" or "Xaa" used: Feature required	Xaa Cys Xaa Cys Xaa Xaa Xaa Cys Cys Ser A
193	W	"N" or "Xaa" used: Feature required	Xaa
240	W	"N" or "Xaa" used: Feature required	Xaa Xaa Cys Xaa Xaa Phe Xaa Cys Thr Xaa S
242	W	"N" or "Xaa" used: Feature required	Ser Cys Asp Trp Thr Tyr Cys Xaa Leu Xaa
256	W	"N" or "Xaa" used: Feature required	Asp Cys Thr Ser Xaa Phe Gly Arg Cys Thr V
258	W	"N" or "Xaa" used: Feature required	Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa L
272	W	"N" or "Xaa" used: Feature required	Xaa Leu Xaa Cys Ser Val Xaa Phe Ser His C
274	W	"N" or "Xaa" used: Feature required	Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr C
276	W	"N" or "Xaa" used: Feature required	Asp Xaa
289	W	"N" or "Xaa" used: Feature required	Xaa Xaa Arg Xaa Gly Gly Cys Met Ala Xaa P
291	W	"N" or "Xaa" used: Feature required	Asp Ser Xaa Cys Cys Ser Asn Ser Cys Asp V
293	W	"N" or "Xaa" used: Feature required	Met Xaa Phe Xaa Xaa Asp Xaa
305	W	"N" or "Xaa" used: Feature required	Cys Lys Thr Tyr Ser Lys Tyr Cys Xaa Ala A
307	W	"N" or "Xaa" used: Feature required	Xaa Gln Cys Val Arg Ser Tyr Cys Thr Leu P
321	W	"N" or "Xaa" used: Feature required	Asp Xaa Xaa Asp Asp Gly Cys Ser Val Xaa G
323	W	"N" or "Xaa" used: Feature required	Ala Xaa Cys Cys Ser Gly Asp Cys His Xaa T
325	W	"N" or "Xaa" used: Feature required	Xaa Val
338	W	"N" or "Xaa" used: Feature required	Gly Met Xaa Gly Xaa Cys Lys Asp Gly Leu T
340	W	"N" or "Xaa" used: Feature required	Ser Xaa Cys Cys Ser Xaa Asp Cys Xaa Gly S
353	W	"N" or "Xaa" used: Feature required	Xaa Cys Arg Ala Xaa Tyr Ala Xaa Cys Ser X
369	W	"N" or "Xaa" used: Feature required	Asn Gly Gln Cys Xaa Asp Val Xaa Met Xaa C
371	W	"N" or "Xaa" used: Feature required	Cys Cys Ser Leu Asp Cys Xaa Met Tyr Cys T
384	W	"N" or "Xaa" used: Feature required	Cys Gly Gly Xaa Ser Thr Tyr Cys Xaa Val A
386	W	"N" or "Xaa" used: Feature required	Xaa Ser Cys Val Arg Ser Tyr Cys Thr Leu P
399	W	"N" or "Xaa" used: Feature required	Asn Gly Gly Cys Lys Ala Thr Xaa Met Ser C
579	W	"N" or "Xaa" used: Feature required	ctctgccggt tgacacntca tctactctct cagtctcc
800	W	Invalid/Missing Amino Acid Numbering	
831	W	"N" or "Xaa" used: Feature required	Leu Cys Xaa Asp Tyr Thr Xaa Xaa Cys Ser H
833	W	"N" or "Xaa" used: Feature required	Ser Xaa Asn Cys Tyr Asn Gly His Cys Thr
847	W	"N" or "Xaa" used: Feature required	Xaa Cys Cys Ser
866	W	"N" or "Xaa" used: Feature required	sartgytgyt cn
886	W	"N" or "Xaa" used: Feature required	athytnytng tngcngcngt nytn
898	W	"N" or "Xaa" used: Feature required	Asp Cys Thr Ser Trp Phe Gly Arg Cys Thr V
900	W	"N" or "Xaa" used: Feature required	Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa L
912	W	"N" or "Xaa" used: Feature required	Cys Gly Gly Tyr Ser Thr Tyr Cys Xaa Val A
925	W	"N" or "Xaa" used: Feature required	Asp Xaa Thr Ser Trp Phe Gly Arg
938	W	"N" or "Xaa" used: Feature required	Xaa Thr Val Asn Ser Xaa Xaa Xaa Ser Asn S
940	W	"N" or "Xaa" used: Feature required	Xaa Xaa Leu Tyr Ala Phe Xaa Ser